

SEQUENCE LISTING

<110> AMANO, Yuichiro
SUGIYAMA, Yasuo
NISHIDA, Mayumi
TAKETOMI, Shigehisa

<120> Disease Model Animal Carrying Heterologous PPAR Alpha Gene Introduced
Thereinto And Use Thereof

<130> 2005-0041A/WMC/00279

<140> 10/521,174

<141> 2005-1-14

<150> JP 2002-206162

<151> 2002-07-15

<160> 9

<170> PatentIn version 3.1

<210> 1

<211> 1404

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1404)

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Gly Asp Leu Glu Ser Pro Leu Ser Glu Phe Leu Gln Glu Met Gly	
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aac atc caa gag att tcg caa tcc atc ggc gag gat agt tct gga agc	144
Asn Ile Gln Glu Ile Ser Gln Ser Ile Gly Glu Asp Ser Ser Gly Ser	
35 40 45	
ttt ggc ttt acg gaa tac cag tat tta gga agc tgt cct ggc tca gat	192
Phe Gly Phe Thr Glu Tyr 55 Tyr Leu Gly Ser Cys Pro Gly Ser Asp	
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ggc tcg gtc atc acg gac acg ctt tca cca gct tcg agc ccc tcc tcg	240
Gly Ser Val Ile Thr Asp Thr Leu Ser Pro Ala Ser Ser Pro Ser Ser	
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gtg act tat cct gtg gtc ccc ggc agc gtg gac gag tct ccc agt gga	288
Val Thr Tyr Pro Val Val Pro Gly Ser Val Asp Glu Ser Pro Ser Gly	
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gca ttg aac atc gaa tgt aga atc tgc ggg gac aag gcc tca ggc tat	336
Ala Leu Asn Ile Glu Cys Arg Ile Cys Gly Asp Lys Ala Ser Gly Tyr	
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cat tac gga gtc cac gcg tgt gaa ggc tgc aag ggc ttc ttt cgg cga	384
His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly Phe Arg Arg	
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acg att cga ctc aag ctg gtg tat gac aag tgc gac cgc agc tgc aag	432
Thr Ile Arg Leu Lys Leu Val Tyr Asp Lys Cys Asp Arg Ser Cys Lys	
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atc cag aaa aag aac aga aac aaa tgc cag tat tgt cga ttt cac aag	480
Ile Gln Lys Lys Asn Arg Asn Lys Cys Gln Tyr Cys Arg Phe His Lys	
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Cys Leu Ser Val Gly 165 Met Ser His Asn Ala 170 Ile Arg Phe Gly 175 Arg Met	
cca aga tct gag aaa gca aaa ctg aaa gca gaa att ctt acc tgt gaa	576
Pro Arg Ser Glu 180 Lys Ala Lys Leu Lys 185 Ala Glu Ile Leu Thr 190 Cys Glu	
cat gac ata gaa gat tct gaa act gca gat ctc aaa tct ctg gcc aag	624
His Asp Ile 195 Glu Asp Ser Glu Thr 200 Ala Asp Leu Lys Ser 205 Leu Ala Lys	
aga atc tac gag gcc tac ttg aag aac ttc aac atg aac aag gtc aaa	672
Arg Ile Tyr Glu Ala Tyr Leu 215 Lys Asn Phe Asn Met 220 Asn Lys Val Lys	
gcc cgg gtc atc ctc tca gga aag gcc agt aac aat cca cct ttt gtc	720
Ala Arg Val Ile Leu Ser 230 Gly Lys Ala Ser Asn 235 Asn Pro Pro Phe Val 240	
ata cat gat atg gag aca ctg tgt atg gct gag aag acg ctg gtg gcc	768
Ile His Asp Met Glu Thr Leu Cys Met Ala 250 Glu Lys Thr Leu Val 255 Ala	
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Lys Leu Val Ala Asn Gly Ile Gln Asn Lys Glu Ala Glu Val 270 Arg Ile	
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Phe His Cys 275 Cys Gln Cys Thr Ser 280 Val Glu Thr Val Thr 285 Glu Leu Thr	
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Glu Phe Ala Lys Ala Ile Pro 295 Gly Phe Ala Asn Leu 300 Asp Leu Asn Asp	
caa gtg aca ttg cta aaa gga gtt tat gag gcc ata ttc gcc atg	960
Gln Val Thr Leu Leu Lys 310 Tyr Gly Val Tyr Glu Ala Ile Phe Ala Met 320	
ctg tct tct gtg atg aac aaa gac ggg atg ctg gta gcg tat gga aat	1008
Leu Ser Ser Val Met Asn Lys Asp Gly Met 330 Leu Val Ala Tyr Gly 335 Asn	
ggg ttt ata act cgt gaa ttc cta aaa agc cta agg aaa ccg ttc tgt	1056
Gly Phe Ile Thr Arg Glu Phe Leu Lys 345 Ser Leu Arg Lys Pro 350 Phe Cys	
gat atc atg gaa ccc aag ttt gat ttt gcc atg aag ttc aat gca ctg	1104
Asp Ile Met Glu Pro Lys Phe Asp Phe Ala Met Lys Phe Asn Ala Leu	
gaa ctg gat gac agt gat atc tcc ctt ttt gtg gct gct atc att tgc	1152
Glu Leu Asp Asp Ser Asp Ile Ser Leu Phe Val Ala 380 Ala Ile Ile Cys	
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Cys Gly Asp Arg Pro Gly Leu Leu Asn Val Gly 395 His Ile Glu Lys Met 400	
cag gag ggt att gta cat gtg ctc aga ctc cac ctg cag agc aac cac	1248
Gln Glu Gly Ile Val His Val Leu Arg Leu His Leu Gln Ser Asn His	
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Cys	Leu	Ser	Val	Gly	Met	Ser	His	Asn	Ala	Ile	Arg	Phe	Gly	Arg	Met
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Pro	Arg	Ser	Glu	Lys	Ala	Lys	Leu	Lys	Ala	Glu	Ile	Leu	Thr	Cys	Glu
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Gly	Phe	Ile	Thr	Arg	Glu	Phe	Leu	Lys	Ser	Leu	Arg	Lys	Pro	Phe	Cys
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Gln	Glu	Gly	Ile	Val	His	Val	Leu	Arg	Leu	His	Leu	Gln	Ser	Asn	His
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Pro	Asp	Asp	Ile	Phe	Leu	Phe	Pro	Lys	Leu	Leu	Gln	Lys	Met	Ala	Asp
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Leu	Arg	Gln	Leu	Val	Thr	Glu	His	Ala	Gln	Leu	Val	Gln	Ile	Ile	Lys
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